

Figure 2A

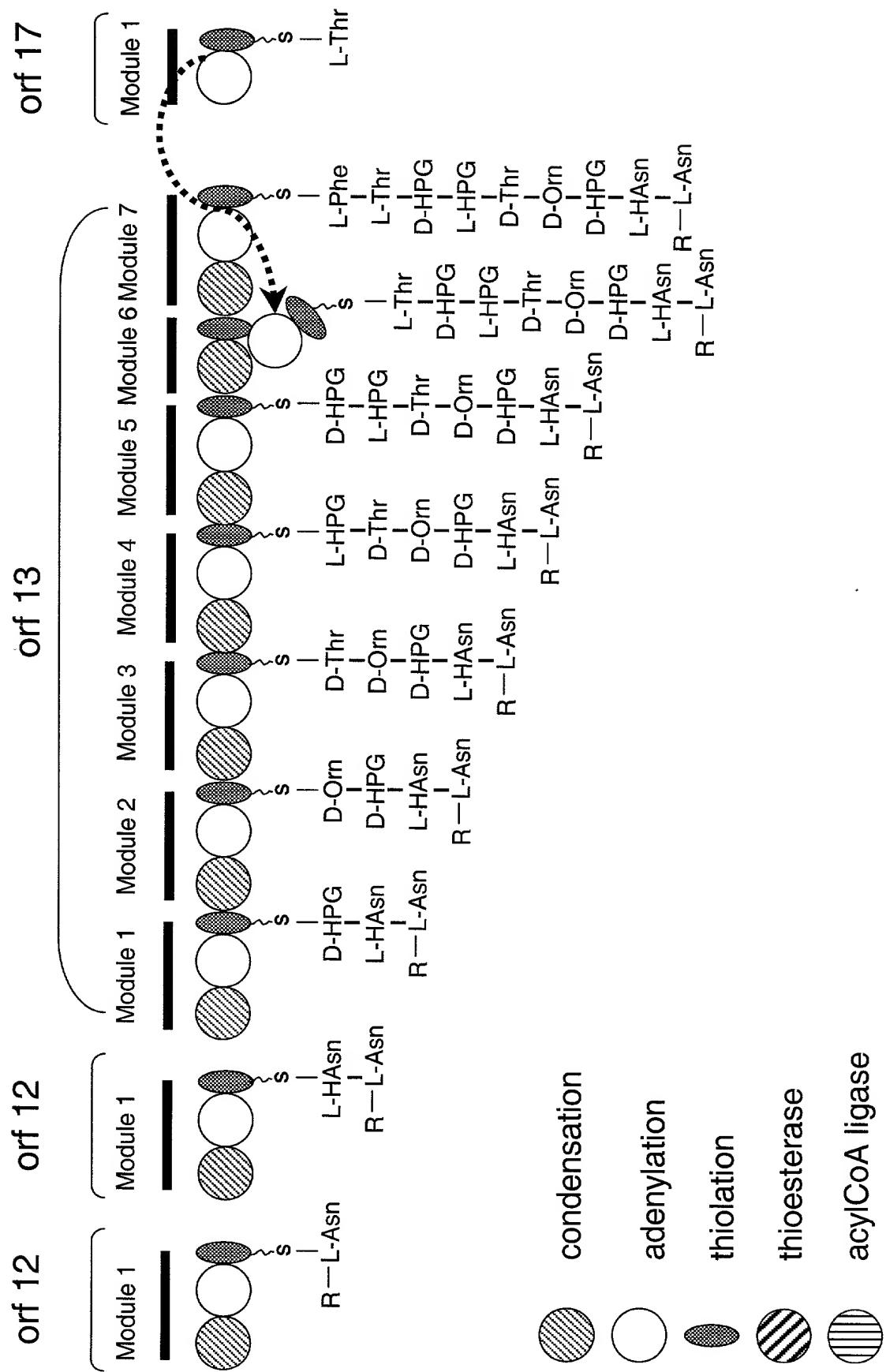


Figure 2A cont'd

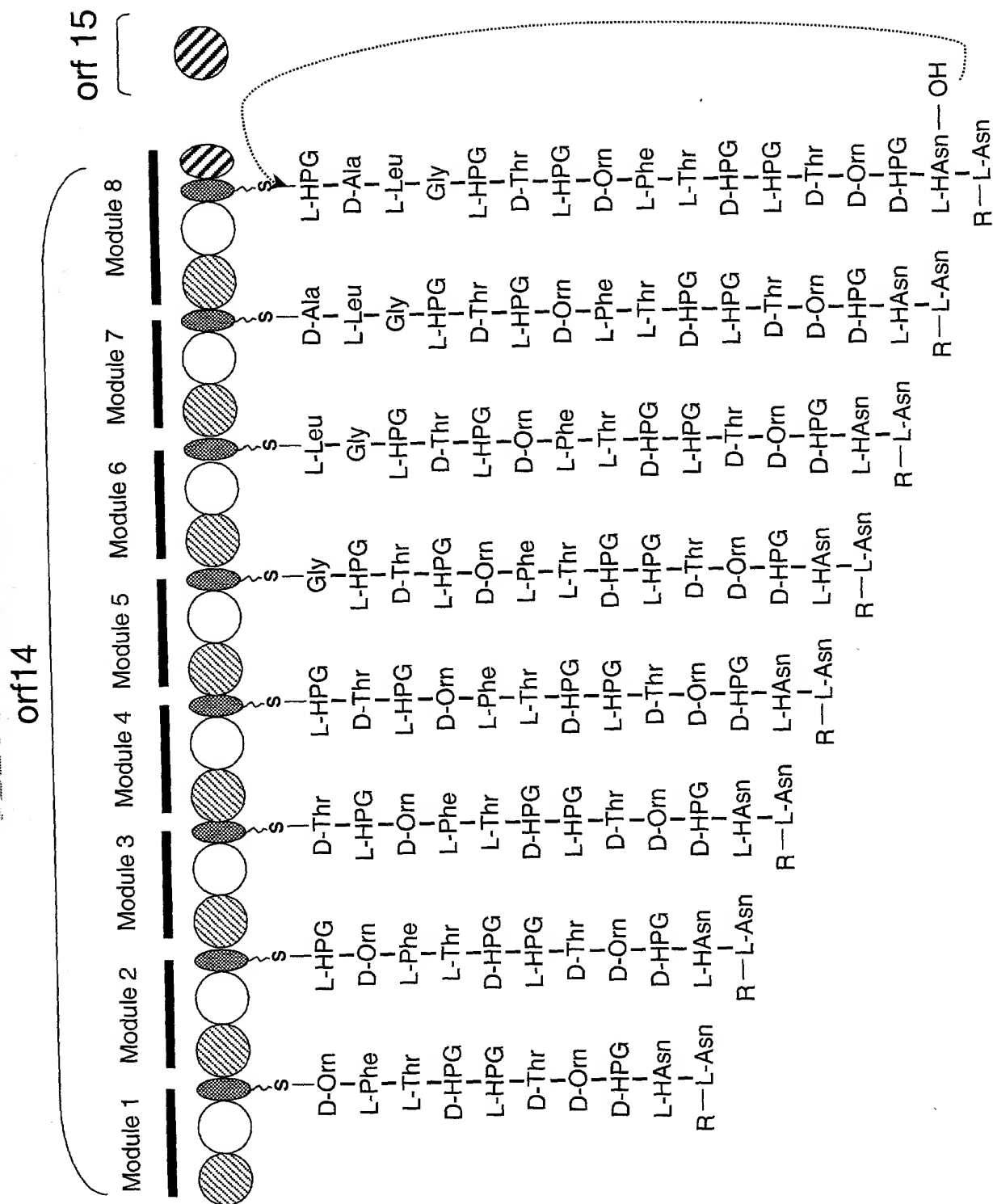


Figure 2B

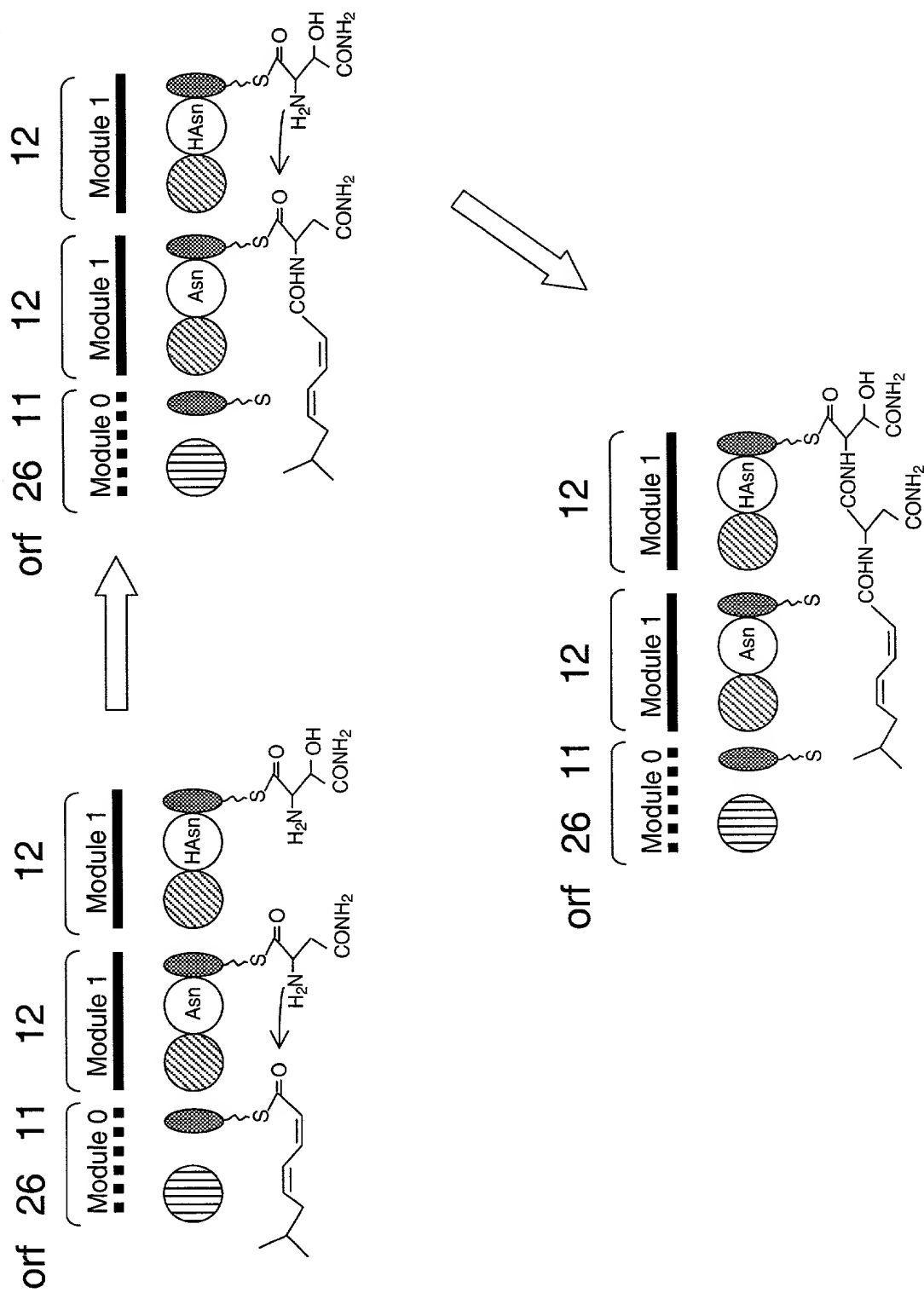


Figure 2C

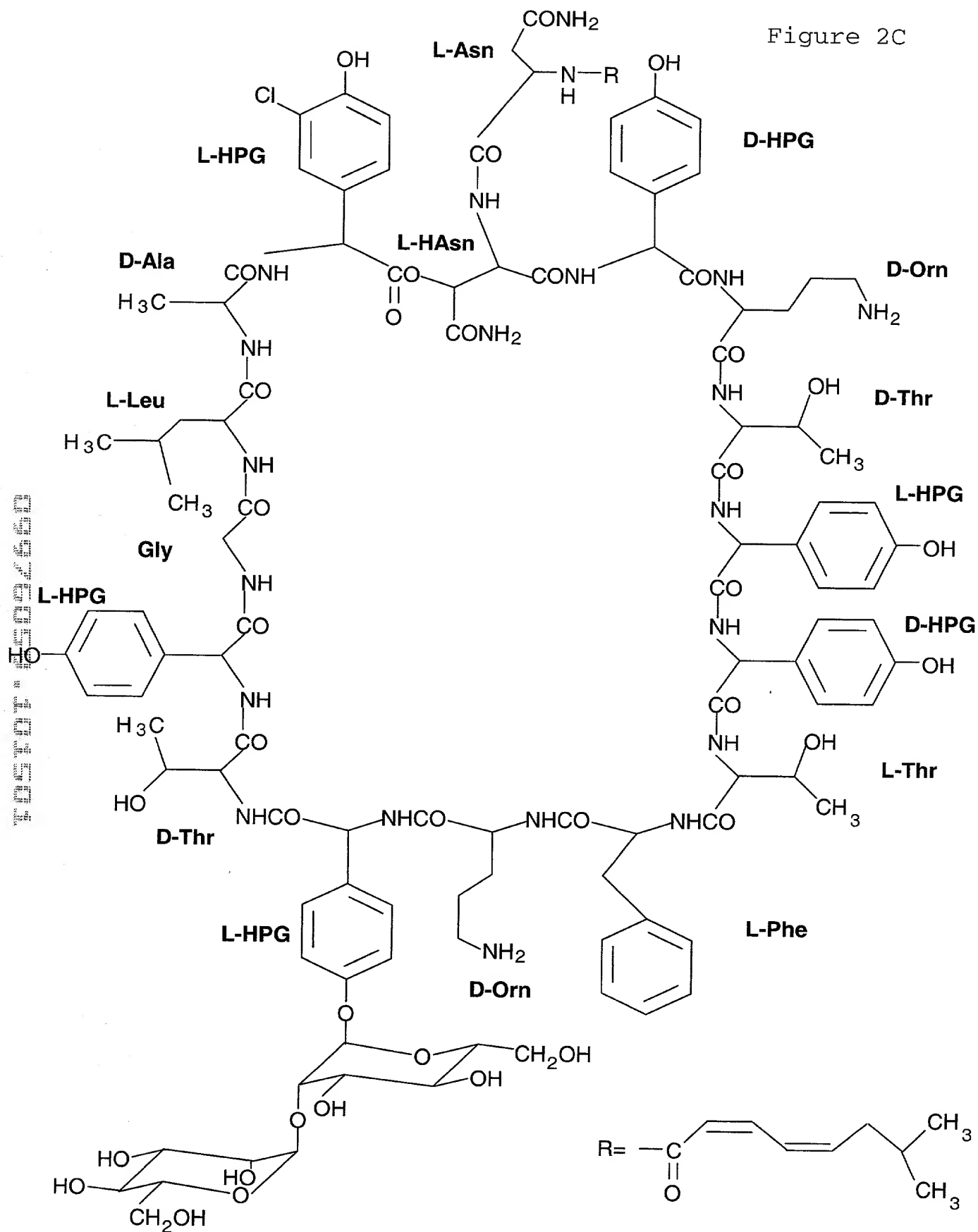


Figure 3A

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Orf12 -----ERRRLLEDEWN-ATAAPSSDTVLARFEEQAARTPEAPAVVC
Orf13 |M1 -----ERSRLLEWENDTARPVVLESSVPALFAKRVAATPDATAVVG
Orf13 |M2 -----NATAVPAQPALVPELFTAQAARTPTWPAVLT
Orf13 |M3 -----DRLLTAWNEAREPAPP-VTLPDFDRQARRTPBAVALTA
Orf13 |M4 -----EIERVVHSWNDTARPVVLESSVPALFAEQVAAAPDATAVVG
Orf13 |M5 -----ERSRLLEWENDTARPVVLESSVPALFAEQVAAAPDATAVVG
Orf13 |M7 -----TVPELVAAQVARRPGAVALRS
Orf14 |M1 -----NDTAAPAPAGLVPDFLFAAQAARTPDAAVAVAG
Orf14 |M2 -----NDTARRVRQASVPELFAERVAAAPGAPAVAA
Orf14 |M3 -----EESRLMLAAGEEPAPALPEITVAALVAEQCARTPGAVAVTG
Orf14 |M4 -----NETRRAVTRASVPELFAKQVAATPDAAVAVAG
Orf14 |M5 -----ERRLVLTGWNDTAAVPAVAVPELIERRAAAEPEAGAVVC
Orf14 |M6 -----ERREVLRTPNATARDVAAATLPAIVGEWARTTPGATAVTA
Orf14 |M7 -----EREAVLSGGNGGTAPVPVTTVPALFAEQARRTPGAVAAALS
Orf14 |M8 -----ERSRLLEWENDTARPVVLESSVPALFAERVAAAPDATAVVG
Orf17 -----RTLTLGLFAEQVAARPTAVAVSD
GrsA_Adomain MLNSSKSILIIHAQNKNGTHEEEQYLFVNNTKAEYPRDKTIHQLFEEQVSKRPNNVAIVC

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A1 A2
Orf12 GDVVTYAELEAGANRLARVLRARGAGPESVVALCLPRGPEVVTGILAAWKAGAAAYLPVD
Orf13 |M1 EGVSWSYRELDRRSDVLARRLVAAGVGVEPVVVALERSPEVLSAFLAVAKAGGVFVFPVD
Orf13 |M2 AGAEMSYAELEERSNRLARWLARGRGVADDRVALMMRRGPELMVAAILAVLKAGAAAYLPVD
Orf13 |M3 DGVSLTYRELSERANRIARLLTSRGIGFESLVGVVLRPSADLVVALLGVQAGAAAYVPVD
Orf13 |M4 EGVSWSYRELDARSDALARSLVAAGVGVEPVVVALERSPEVLSAFLAVAKAGGVFVFPVD
Orf13 |M5 EGVSWTYRELDARSDALARSLVAAGVGVEPVVVALERSPEVLSAFLAVAKAGGVFVFPVD
Orf13 |M7 EDGEITYAELEARAGRLAAVLRRRRGIGPESRVAVLLPRGVEQVVAFLAVVRAGGTYPID
Orf14 |M1 PDREITYAELEDERSGRLARWLIRRGVAADTRVALVLESAELPVAILAVLKAGGAYLPID
Orf14 |M2 GDLRWTYADLDARSDALARSLVAAGVTAESPVVVALERSADVLTAFLAVAKAGGVFVFPVD
Orf14 |M3 PDASITYAELEDERAARIARWLRRHGAGPGAACVLMERSAELVAVLLGVMRAGAAAYVPVD
Orf14 |M4 EGVSWSYRELDVRSDALARSLVAAGVGIESPVVVALDRSPEVPTAFLAVAKAGGVFVFPVD
Orf14 |M5 GDTMLRYGELNARANRLARLLVERGAGPESIVAVCLERSADLVVTLAVLKAGAAAYLPID
Orf14 |M6 ENDRITYAELEARANRLARSLIARGVGPGAVVGMLLRSPGLVVAAMLATVKAAGAYLPID
Orf14 |M7 EGMSLTYADLAARVNRLARHLVSLGAGPETVVGIIAMSRGLDMLVAVLAVQAGAAAYLPVD
Orf14 |M8 EGVSWSYRELDRRSDVLARSLVAAGVGLESPVVVALERSADVLTAFLAVAKAGGVFVFPVD
Orf17 DRGRHTYRELDWMSGRLARGLRKAGVRDGDVGVCLDRSAELVAVLLAVLKAGAAAYVPID
GrsA_Adomain ENEOLTYHEINVKANQLARIFIEKGIGKDTLVGIMMEKSIDLFIGILAVLKAGGAYVPID

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Orf12 TELPAERVAYLLGDSAAAVRLG--TAETLAALPDGP-----AADVDVHA
Orf13 |M1 LSWPQARVDVAVDCAARVAVA--DRPMSGLTVVSAGL-----GGDSAVVSA
Orf13 |M2 PDLPRDRVDYLLADAAPAFVLA--ERATAPWVPVA-----GGIPVLVVDA
Orf13 |M3 ADYPAERIGYILGDAGAVCVLT--VDTAGAVPPG-----VPKLVLDH
Orf13 |M4 LSWPQARIDAVVADCAARVAVA--DRPMSGLTVVPA-----GGDSAVVSG
Orf13 |M5 LSWPQARVDVAVDCAARVAVA--DRPMSGLTVVSAGL-----GGDSAVVSG
Orf13 |M7 PAYPRDRVDYLRDAEPACLLT--VAGHRAAFAAP-----AVVELDD
Orf14 |M1 PAQPPRIADIVADAAPALVLA--QASTADVADASPALVLPASDGVPTGAVPVHLLDS
Orf14 |M2 LSWPRARVDVAVDCAAWIAVA--DRPMTGLTVVPAN-----VPCLAIDD
Orf14 |M3 PAYPAERIRFVVTDARAACVVS--ESASAGLVDPG-----VPCLAIDD
Orf14 |M4 LSWPQARVDVAVDCAARVAVA--DRPMTGLTVVPA-----VPCLAIDD
Orf14 |M5 PGYPAGRIAYMLADARPALLVTSPAVASGDSLDPGG-----AQRIVLGD
Orf14 |M6 PGYPAPRLARMVEDAAPALLLA--TAGTADAVPAGP-----QRLLLDD
Orf14 |M7 PSYPDERKEFMLTDAGAAVYLT--LASDADRVPFGTP-----AAAVVLDE
Orf14 |M8 LSWPQTRIDAVIAD-S-----RPVLVLDSDVLDL-----AAAVVLDE
Orf17 AAYPADRIAYTVGDAGLAVVVT--TSADFDPV-DG-----VRLAPES
GrsA_Adomain IEYPKERIQYILDDSQARMLLT--QKHLVHLIHNQFN-----GQVEIFEE

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Figure 3A

A3

Orf12		PEIARE-----SP-----SPLRLPLELPDQLAYVIYTSGSTGLSKGVGVSHGGLANYVGVAS
Orf13	M1	DLTADRAVVLPSRPVP-----GAAVYRMYTSGSTGRPKGVVTHQNLDLAT---
Orf13	M2	PAVAEEVAHSGEAVTDRDRRAALRGGHAYVIYTSGSTGRPKGVLI THDGLANLTL-DH
Orf13	M3	PETVTALAACDTAPLGEAERAGELLPEHPAYVIYTSGSTGTPKGVLI PHRNVLFAATR
Orf13	M4	DQVGDSAVVLPA GPVP-----GAAVYRMYTSGSTGRPKGVVTHQNLDLAT---
Orf13	M5	DLTADRAVVLPA GPVP-----GAAVYRMYTSGSTGRPKGVVTHQNLDLAT---
Orf13	M7	PATAAEIADAEPEPP-----VAVRPTH SAYLIYTSGSTGRPKGVVTHRGVAALVATQA
Orf14	M1	PAVRDEVAQC PAGAVTDADRRGVLLGGHAAVVIYTSGSTGRPKGVVSHDAFANLVL-DQ
Orf14	M2	-RAGDPAVALPPRPLP-----GAAVYRMYTSGSTGRPKGVVTHQNVDLVT---
Orf14	M3	P-----AAAAEPAEPGDDPGDAAGPRPDPAYIIYTSGSTGTPKGVVSHRNVALLTATR
Orf14	M4	DAAGDPAAEPLPPRPLP-----GAEVYRMYTSGSTGRPKGVVTHQNLDLAT---
Orf14	M5	PDTAALDGLAGTDLVLSERRGVTHPAHPAYVIYTSGSTGRPKGVVPHGALTNFVAAMS
Orf14	M6	PGTAAELARLDGDPIDREERTHLRPGHPAYLMFTSGSTGRPKGVLPVPHAGIDRMVR-RS
Orf14	M7	PVTAARIAGLDPADLTDADRVAPLLPAHRAVVIYTSGSTGRPKGVAVEHRTVNNLSWAA
Orf14	M8	-----AAEADLPRVPA-----GAGVYRMYTSGSTGRPKGVVTHQNLDLAT---
Orf17		-----LAEAGDDPGIPLATPAG--PERPAYVIYTSGSTGRPKGVVPHANVSALLDATR
GrsA_Adomain		DTIKIREGNTLHVPSK-----STDLAYVIYTSGTTGNPKGTMLEHKGISNLKVFFE

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A4

Orf12		VLYGGLSAP---LHSSLAFDLTVTSVFPVPLVCGGSVVVSAAGGGRGLASLLAAGDG--FS
Orf13	M1	-DTCWGPTPRVLFHAPHAFDASSYEIWVPLLNGGTVVVAPQRSID-ATVLRDLIRAHDLT
Orf13	M2	GRFGLGPGARVAQFASPGFDMFVDEWSMALLAGAALTFFVPPERRL-GADLAAFLAEYGV
Orf13	M3	GSPHFGEQDVWSWFHSAFDFEISVWELWGALLHGGRVVMVFAVSRSPRDFWELLVREVT
Orf13	M4	-DTCWGPTPRVLFHAPHAFDASSYEIWVPLLNGGTVVVAPQRSID-ATVLRDLIRGHELT
Orf13	M5	-DTCWGPTPRVLFHAPHAFDASSYEIWVPLLNGGTVVVAPRRSID-ATVLRDLIGAHELT
Orf13	M7	ERLAVTGESRVLQFASVGFDAISIWEMVMALCAGATLVVAPADDLLPGPALAATLSGHA
Orf14	M1	RRLGIGPGSRVAQFASPGFDMFVDEWSMALLAGALVIVPPERRL-GADLAAFLTERGVT
Orf14	M2	-DRCWGPTPRVLFHAPHAFDASSFELWVPLLTTGGTVVVPAGESID-TGVLRLQIRAH
Orf14	M3	PLFGFAGDEVWSWFHSAFDFEISVWELWGALT HGGRVVPVYAVSRSPRDFWELVRE
Orf14	M4	-DTCWGPTPRVLFHAPHAFDASSYEIWVPLLNGGTVVVAPGRSID-AAVLGELIRAH
Orf14	M5	DRLALGAGDRLLAVTTVAFDITVLELYVPLVGGAGVVVAEDAVVRDPAVAALDRH
Orf14	M6	TCLQLAPDDVLPPLSSVSFDAATFEIWGALLNGATLAVAPAETLS-VAELRAFLADR
Orf14	M7	GRFGGADFARTLAATSLNFDVSVFEIFGPLVSGGSIEIVTDLLALADPASPAWEA----
Orf14	M8	-DTCWGPTPRVLFHAPHAFDASSYEIWVPLLNGGTVVVAPRRSID-ATVLRDLVRGHELT
Orf17		EEYALGPGDVWVTFHSAFDFEISVWELWGCLLTGGHLVVPYVWVSRSPQFHDLLAERG
GrsA_Adomain		NSLNVTEKDRIGQFASISFEDASVWEMFMALLTGASLYIILKDTINDFVKFEQYINQ

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A5

Orf12		LVKVVPGLRLLLAELVPAGEMA AVG----SLVAGGEVLAGGDVREWLSRVPGS--VVVNE
Orf13	M1	HVHVTA---GLLRVL---DPSCFAG--LTEVLTGGDAVSAEAVRRVKDANPGL--RVRQL
Orf13	M2	HATLPP---AVVGITPDGVLPPSF----VLDPVGGDVLPGLDARR--WLRDGR--VIFNS
Orf13	M3	VLSQTP---SAFYQLAAAA-DDTPD-ALRVVVEGGEALDPGRLAGWRERRPDG-PRIVNM
Orf13	M4	HVHVTA---GLLRVL---DPSCFAG--LTEVLTGGDAVSAEAVRRVREANPGL--RVRQL
Orf13	M5	HVHVTA---GLLRVL---DPSCFAG--LTEVLTGGDAVSAEAVRRVKDANPGL--RVRQL
Orf13	M7	HATLPP---AVLAASAPGDLAPLA----VLVSAGEALGPDLVR--QFAPGR--AIVNA
Orf14	M1	HATLPP---AVVATLPEESLERSF-----VLDPGGDALPDDLARR--WLRDGR--WLGNS
Orf14	M2	HVHVTA---GLLRVLA E-DPSCFAG--LTEVLTGGDVVPAAEAVRRVLDANPGV--RVRQL
Orf14	M3	VLSQTP---SAFAQLMAAAGDDDRD-ALRFVVEGGEALDPGRLAGWLARRPDK-PRIVNM
Orf14	M4	HVHVTA---GLLRVL---DPSCFAG--LTEVLTGGDAVSAEAVRRVMEANPGL--RVRQL
Orf14	M5	IVQATP---ALWQALLAGHADAVRD---VRLVVGGEALPPALAG--RMAAAGR--GVTNL
Orf14	M6	KLFLTT---GLLHEVIDADVTALAG--LKAVYTGDDVLSPAHCRSLLD RVPGL--EITYNA
Orf14	M7	LVSGVP---SAFSRVLDRGDIAART---RSVVLAAGEALTADVNNATRAALPGV--RVAN
Orf14	M8	HVHVTA---GLLRVL---DPSCFAG--LTEVLTGGDAVSAEAVRRVKEANPGL--RVRQL
Orf17		VLNQTP---SSTQLVAADRGAERDLAVRLVIEGGEPLDARTVLPWLD RRPPEARCRIVNM
GrsA_Adomain		VITLPP---TYVVHLDPERILSIQT-----LITAGSATSPSLVNKWEKVT-----YINA

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Figure 3A cont'd (2)

A5A6

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Orf12      YGPTETTVVGC SVFSVAAGDVVGD--VVPVGRPVANTRLFVLDEGLRPVPAGVAGELYVAG
Orf13 |M1   YGPTETVTL CATQHLLD-DG-----VPIGRPLDNTRVYVLDLQLQVPVPGVGTGELYVAG
Orf13 |M2   YGPTETTVNAATWR-AEAGDWGS--VAPIGTPVPNL RAYVLDGWL RPVPVGDGELYVSG
Orf13 |M3   YGITEHTTVHVTHQDLAPAD-TTG--S-PIGRGIPGLSVYVLDALRPVPPGVAGEVYVAG
Orf13 |M4   YGPTETVTL CATQHLLV-DG-----VPIGRPLDNTRVYVLDLQLQVPVPGVGTGELYVAG
Orf13 |M5   YGPTETVTL CATQHLLD-DG-----VPIGRPLDNTRVYVLDLQLQVPVPGVGTGELYVAG
Orf13 |M7   YGPTETTVCATASAPLGPEDPPH----IGAPVADSRVYVLDLALTPVPPGVGTGELYVSG
Orf14 |M1   YGPTETTVNAATWR-CEPGTWEG--ATPIGRPVANL RAYVLDGRL RPVPVPGVGTGELYVSG
Orf14 |M2   YGPTETVTL CATQHVVREPSPV----LPPIGRPLDNTRVYVLDGLLQVPVPGVGTGELYIAG
Orf14 |M3   YGITEHTTVHTTYQHIA PG--TTG--S-VIGRGLPGFGLYVLDALRPVPAGVPGEVYARG
Orf14 |M4   YGPTETVTL CATQQVLDGTG-----VPIGRPLDNTRVYVLDLQLQVPVPGVGTGELYVAG
Orf14 |M5   YGPTETTVWATVADLGA-SPAG---FVPIGTPLRNTRAFVLDLALRPVPPGVGTGELYLAG
Orf14 |M6   YGPTENTTTITLHR-VRPEDLDAGTGVPVIGVPI SDTRVYVLDLALRPVPVPGVAGELYTSG
Orf14 |M7   YGPTETTVYSTAWHTDR-DVTGG--AAPIGRPVTNTRAYVLDLRLTPVPPGVGTGELYLAG
Orf14 |M8   YGPTETVTL CATQHLLD-DG-----VPIGRPLDNTRVYVLDLQLQVPVPGVGTGELYVAG
Orf17      FGITEHTTVHVTAVDVTRAAALAG--SRSVGRPLPGWAVRVLDEQRREVPPGVPGEIYVGG
GrsA_Adomain YGPTETTTICATTWATKETIGHS---VPIGAPIQNTQIYIVDENLQLKSVGHAGELCIGG
          : * * * . : : * : . : * : . * * * : *

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A6A7A8

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Orf12      SQVARGYVGRSGLTASRFVACPFPG-VGERMYRTGDLVRVLAG-GDLVFPVGRVDEQVKIRGY
Orf13 |M1   AGVARGYAGMPGLTAERFVADPFNT--GGRLYRTGDLVRWTDGVLHFAGRADDQVKIRGY
Orf13 |M2   AGLARGYLNRAGLTAERFVACPFEP-GERMYRTGDLVRWTAEGRLVFAGRSDDQVKIRGF
Orf13 |M3   RQLARAYLGRAALTGTRFVACPFPLPAGERMYRTGDRARWSR--GRLQFAGRTDDQVQIRGF
Orf13 |M4   AGLARGYAGMPGLTAERFVADPFSS--GGRLYRTGDLVRWTDGVLHFAGRADDQVKIRGY
Orf13 |M5   SGLARGYAGMPGLTAERFVADPFNT--GGRLYRTGDLVRWADDGVLHFAGRADDQVKIRGY
Orf13 |M7   ASLARGYAGRAALTAE RFVACPFAP-GERMYRTGDRARWDAAGRLTFAGRADDQVKIRGF
Orf14 |M1   AGLARGYLNRAGLTAGSFVACPFEP-GERMYRTGDLVRWDARGRLVYAGRADDQAKIRGF
Orf14 |M2   AGVARGYADMPGTTAERFVADPF TA--GGRLYRTGDLVRWTEGEGELVFAGRADDQVKIRGY
Orf14 |M3   PQVARGYIGRPGLTAERFVADPFAP--GERMYRTGDLVRWTDGRLVFAGRSDDQVKIRGF
Orf14 |M4   AGLARGYAGMPGLTAERFVADPFSS--GGRLYRTGDLVRWTDGVLVFAGRADDQVKIRGY
Orf14 |M5   DQLARGYHGRAGLTAE RFVADPFPG--RGERMYRTGDRVRWTRGGSLEFLGRVDDQVKIRGF
Orf14 |M6   IGLAHGYAGRPAPTAE RFVACPFAP--GERMYRTGDLVRWTDGRLVFAGRADNQVKIRGF
Orf14 |M7   AQLARGYLGRPGLTGERFVACPFPGGGERMYRTGDRVRWNADGDLVFAGRADDQVKIRGF
Orf14 |M8   SGLARGYAGMPGLTAERFVADPFSS--GGRLYRTGDLVRWTDGVLHFAGRADDQVKIRGY
Orf17      AGVAIGYLNRP ELTAERFVTG---PDGRRWYRSGDRGRLLPDGTLEHLGRLLDQVKIRGF
GrsA_Adomain EGLARGYVWRPELT SQKFVDNPFVPG--GEKLYKTGDDARWLS DGNIEYLGRLDQVKIRGF
          : * * . * . * * * : * : * : * * : * : . * * * : * : * : *

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A8A9

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Orf12      RVEPDEVHLLVVAGHPRVAGAAVVARPDVAGE---RQLVAYVVVPAAGEPAG---LAESVRAH
Orf13 |M1   RVEPGEVHAVLAQHDPDVSQVAVVVREDTPGD---KRLVAYVVVGG-----DIEAY
Orf13 |M2   RIEPGEVHAVLAAGPGV SQA AVIVREDVPGD---KRLVAYVVVGG---D---VEALRSY
Orf13 |M3   RIEPGEVQAVVAHPEIAAAAVVVREDVPGD---PRLTAYVVVPA GPRTAPAAVAETVRRF
Orf13 |M4   RVEPGEVHAVLAQHDPDVSQVAVVVREDTPGD---KRLVAYVVVGG-----DVEAY
Orf13 |M5   RVEPGEVHAVLAQHDPDVSQVAVVVREDTPGD---KRLVAYVVVGG-----DVEAY
Orf13 |M7   RVEPGEVHAVLGEHPAVARA AVVARTDGPQG---ARLVAYLVVADP--AGPDLAAAVRAY
Orf14 |M1   RVEPGEVHAVLAAGPGV NQVAVIVREDVPGD---KRLVAYVVVGG---D---VETLRSY
Orf14 |M2   RVEPGEVHAVLAALPGV SQA AVIVREDVPGD---KRLVAYLVVAAPE-----TVEAARAH
Orf14 |M3   RIEPGEVHAVLAAGPGV SQA AVIVREDVPGD---KRLVAYVVVGG-----DAETLRSH
Orf14 |M4   RVEPGEVHAVLAHDPVAQVAVVVREDTPGD---KRLVAYVVVGG-----DVEAY
Orf14 |M5   RIELGEVHAALAAFGPVARAAA VREDVPGD---RRLVGYVVVPAAGEPE--PDPAAVRAH
Orf14 |M6   RVEPGELEHTVLSGHPA VARAAVLA REDTPGA---KRLVAYVVVPA RPDEDGDALAESVRAY
Orf14 |M7   RIEPGEVQAVVARQAGVARAVVLARS DSPGD---ARLVAYVVVPA DRDADRRA LAATVRS D
Orf14 |M8   RVEPGEVHAVLAQHDPDVSQVAVVVREDAPGD---KRLVAYVVVGG-----DVEAY
Orf17      RIELDEIRGVLTECAGVAAA AVVIRSTPDDPATARLDAYVVVAEAG-----ATPPVAEH
GrsA_Adomain RVELEEVHSILLKHYISETAVSVHKDHQEQ---PYLCAYFVSEKHIP-----LEQLRQF
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Figure 3A cont'd (3)

A10

Orf12	VAERLPEYMPAAVVTLDLPLT	VNGKVDRAALPEP-----
Orf13 M1	GQERLPGYMPVPSAFVHLDALPLT	SNQKVDRAALPAPSMESG-----
Orf13 M2	AQQRLLPGYMPVPSAFVHLDALPLT	VNGKLDRAALPVPDLARG-----
Orf13 M3	AADRLPAYMLPSAVVVLDAALPLT	DHGKLDRAALPAPQHT-----
Orf13 M4	AQERLPGYLVPSAFVHLDALPLT	SNQKVDRAALPAPSVESGV-----
Orf13 M5	AQERLPGYMPVPSAFVQLDALPLT	SNQKVDRAALPAPSMESG-----
Orf13 M7	AAATLPAHLLPAAAFVPLDRLPLT	TNGKLDRAALPEPETGAG-----
Orf14 M1	AQQRLLPGYLVPSAIVALAELPLT	PSAKVDRAALPVPD-----
Orf14 M2	AEQRLLPSYLVPSAFVQLDALPLT	SNQKVDRAALPAP-----
Orf14 M3	AQQRLLPGYLVPSAFVHLDALPLT	VNGKLDRAALPVPD-----
Orf14 M4	AQERLPGYLVPSAFVHLDALPLT	SNQKVDRAALPAPSVESG-----
Orf14 M5	VAAQLPAYMPVPSAVVVLDPDLPLT	TANGKLDRAALPAPDYGAASAGRAPADE--
Orf14 M6	AARQVPDYLMPAATVVLPDLPLT	SSGKVDRAALPAPDVPGG-----
Orf14 M7	TARELPAYLVPAAVVVLDELPLT	TANGKLDRAALPAPGL-----
Orf14 M8	AQERLPGYMPVPSAFVHLEALPLT	ANQKVDRAALPAPE-----
Orf17	AARMLPAYMCPATFTFLDALPMT	PNGKVDRAALPEP-----
GrsA_Adomain	SSEELPTYMIPSYFIQLDKMPLT	SNQKIDRAALPEPDLTFGMRVDYEAPRNE

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09576659 04504

Figure 3B

				235	236	239	278	299	301	322	330	
	Orf13	M1	HPG	D	A	Y	H	L	G	L	L	HPG
	Orf13	M4	HPG	D	A	Y	H	L	G	L	L	
	Orf13	M5	HPG	D	A	Y	H	L	G	L	L	
	Orf14	M2	HPG	D	A	F	H	L	G	L	L	
	Orf14	M4	HPG	D	A	Y	H	L	G	L	L	
	Orf14	M8	HPG	D	A	Y	H	L	G	L	L	
emb	CAB38518.1	Cda1	M6	HPG	D	V	Y	H	L	G	L	
emb	CAA11795.1	CepB	M2	HPG	D	A	V	H	L	G	L	Thr
emb	CAA11795.1	CepB	M1	HPG	D	I	F	H	L	G	L	
	Orf13	M3	Thr	D	F	W	S	V	G	M	V	
	Orf14	M3	Thr	D	F	W	S	V	G	M	V	
	Orf17	M1	Thr	D	F	W	N	I	G	M	V	
gb	AAC38442.1	Acmb	M1	Thr	D	F	W	N	V	G	M	
emb	CAB38518.1	Cda1	M2	Thr	D	F	W	N	V	G	M	
emb	CAA09819.1	FenD	M2	Thr	D	F	W	N	I	G	M	
	Orf13	M2	Orn	D	M	D	T	D	G	S	V	Orn
	Orf14	M1	Orn	D	M	D	T	D	G	S	V	
gb	AAC06347.1	BacB	M1	Lys	D	A	E	S	I	G	S	
gb	AAC82550.1	FxbC	M1	5hOrn	D	M	E	N	L	G	L	
gb	AAC82550.1	FxbC	M3	5hOrn	D	M	E	N	L	G	L	Asn
	Orf12	M1	Asn	D	L	T	K	V	G	E	V	
emb	CAB38517.1	Cda2	M3	Asn	D	L	T	K	V	G	E	
gb	AAC06348.1	BacC	M5	Asn	D	L	T	K	I	G	E	
gb	AAC45930.1	TycC	M1	Asn	D	L	T	K	I	G	E	Phe
	Orf13	M7	Phe	D	A	W	T	V	A	A	V	
emb	CAA33603.1	GrsA	M1	Phe	D	A	W	T	I	A	A	
gb	AAC45929.1	TycB	M3	Phe	D	A	W	T	I	A	G	
gb	AAC06348.1	BacC	M2	Phe	D	A	F	T	V	A	A	Gly
	Orf14	M5	Gly	D	I	L	Q	L	G	L	V	
emb	CAB38517.1	Cda2	M2	Gly	D	I	L	Q	L	G	L	
emb	CAB15186.1	DhbF	M1	Gly	D	I	L	Q	L	G	L	
gb	AAF17280.1	NosC	M2	Gly	D	I	L	Q	L	G	L	Leu
	Orf14	M6	Leu	D	A	F	F	Y	G	A	T	
emb	CAA82227.1	CssA	M2	Leu	D	A	W	L	Y	G	A	
emb	CAA82227.1	CssA	M3	Leu	D	A	W	L	Y	G	A	
gb	AAC06346.1	BacA	M3	Leu	D	A	W	F	L	G	N	(Ala)
	Orf14	M7	(Ala)	D	V	F	S	V	A	I	V	
gb	AAC06348.1	BacC	M2	Phe	D	A	F	T	V	A	A	
gb	AAC83656.1	PchE	M1	Cys	D	L	F	N	L	S	L	
emb	CAA82227.1	CssA	M1	Ala	D	V	F	I	Y	A	A	I

Figure 3C

Orf26
gb|AAB52538.1|acyl_CoA_L|Mb
emb|CAB05426.1|fadD29|Mt
gb|AAG02359.1|blmVI|M1|Sv
gb|AAC44128.1|safB|M1|Mx
gb|AAF08795.1|MycA|M1|Bs

-----MVIDAATQPTVPDAFRAQ
-----MAMSVRSLPAALRAC
MKTNSSFHAAGEVATQPAWGTGEQAAQPLNGSTSRFAMSESSLADLLQKA
-----MSRPAGIVDIARRH
-----MACRPDSLHASAVTSRRRMRHTLVELLQER
-----MYTSQFQTLVDVIRNR
: :

Orf26
gb|AAB52538.1|acyl_CoA_L|Mb
emb|CAB05426.1|fadD29|Mt
gb|AAG02359.1|blmVI|M1|Sv
gb|AAC44128.1|safB|M1|Mx
gb|AAF08795.1|MycA|M1|Bs

AIARPGEPALVVLP--DPDAEPVTLTYAELDRRAAARAALAAARFPAGE
ACLQPHDPAFTFMDYEQDWDGVAITLTWSQLYRRTLNVARELSRCGSTGD
ASQYPNRAAYKFIDYDTPAGFTETVTWQVHRRAMIVAEELWIYASSGD
AERTPARPAYAFPLP---DGETESVRFSPADIDRRARAVAVALQDRGLAGE
ALSEPRHEAFTFLG---EAGVPAVRVDYSSMDVLARAIAARLQADGRVGE
SNIS---DRGIRFIE---SDKIETFVSYRQLFDEAQGFLGYLQHIGIQPK
: . : : : *

ALI

Orf26
gb|AAB52538.1|acyl_CoA_L|Mb
emb|CAB05426.1|fadD29|Mt
gb|AAG02359.1|blmVI|M1|Sv
gb|AAC44128.1|safB|M1|Mx
gb|AAF08795.1|MycA|M1|Bs

R-ILIALPTGAEFVELYLACLYAGLVAVPAPPPGGS--SGASERTVGIAA
R-VVISAPQGLEYYVAVFLGALQAGRIAVPLSVPQGG---VTDERSDSVLS
R-VAILAPQGLEYYIAFMGVLAGLIAVPLPVQPG---IHDERISSALR
R-VLVAYPSGPEYVQAFLGCLYAGVVAVPCDEPR-S--GPSAERLAGIRA
R-ALLLYAPGPEYVAAFFGCLYAGVVAVPPYPPDTARLERSLLRLRTVAR
QEIVFQIQENKSFVVAFWACLLGGMI PVPVSI GEDNDHKLKVRWNIILN
: . : : * : *

Orf26
gb|AAB52538.1|acyl_CoA_L|Mb
emb|CAB05426.1|fadD29|Mt
gb|AAG02359.1|blmVI|M1|Sv
gb|AAC44128.1|safB|M1|Mx
gb|AAF08795.1|MycA|M1|Bs

DCSPALAVVN---ADDAAPLTA-----VLRERGLSGLPVGALPPLAAE
DSSPVAILTTS---SAVDDVVQ---HVARRPGESPPSIIIEVDLLDLDPN
DSAPSIILTTS---SVIDEVTYAPHACAAQGSAPIVVAVDALDLSSSR
DARPALATA---GAPEAGLA-----GLATLDDVAGVDPDAAAG
DSRASVVLTTSFQLGLAGAMFEL-----APELGELSWVATDGIALLAEAG
NPFLLASFTVLDKMKKFAADHD-----LQDPFHQLIEKSDIIQDRIYD
: . : :

AL2

Orf26
gb|AAB52538.1|acyl_CoA_L|Mb
emb|CAB05426.1|fadD29|Mt
gb|AAG02359.1|blmVI|M1|Sv
gb|AAC44128.1|safB|M1|Mx
gb|AAF08795.1|MycA|M1|Bs

AIRPPRGRPRPDSLAVLQYSSSGSTGSPKGVMLSHRAVLANLRAFDRSSGHN
GYTFKEDE-YPSTAYLQYTSGSTRTPAGVVMHQNVVNFQELMSGYFAD
ALDPTRFE-RPSTAYLQYTSGSTRAPAGVVLSHKNVITNCVQLMSDYIGD
AWTDPVAG-PDALAFPLQYTSGSTRRPRGVMVGHGNLLANERCIAAACGHD
AWKPPGLS-GDSVAFPLQYTSGSTADPKGVVLTHRNLMHNLSVIHERFQLN
HPASQYEPEADELAFIQFSSSGSTGDPKGVMLTHNLIHNTCAIRNALAID
* : * : * : * : * : * : *

AL3

Orf26
gb|AAB52538.1|acyl_CoA_L|Mb
emb|CAB05426.1|fadD29|Mt
gb|AAG02359.1|blmVI|M1|Sv
gb|AAC44128.1|safB|M1|Mx
gb|AAF08795.1|MycA|M1|Bs

SDDVF-----GSWLPLHDMGLFAMLTAGLLNGAGVVLMSPTAFVRRPA
TDGI PPPNSALVSWLPPFYHDMGLVIGICAPILGGYPVLTSPVSVFLQRP
SEKVP---STPVSWLPPFYHDMGLMLGIILPMINQDTAVLMSPMFLQRP
RDSTF-----VGWAPFFHDMGLVANLLQPLYLGSLSVLMPPMAFLQRP
RGSRG-----VIWLPFYHDMGLIGGVLTPIFGGLPVDLMSPLSFLQEP
LKDTL-----LSWMLPTHDMGLFACHLVPALAGINQNLMPTELFIRRP
* * * * * : * : * : *

AL4

Orf26
gb|AAB52538.1|acyl_CoA_L|Mb
emb|CAB05426.1|fadD29|Mt
gb|AAG02359.1|blmVI|M1|Sv
gb|AAC44128.1|safB|M1|Mx
gb|AAF08795.1|MycA|M1|Bs

DWLRRMDRYRVTLSAAPNFAYDLCVRAVRDEQIAGLDLSRIRTLYNGSEP
RWMHLMASDFHAFSAAPNFAFELAAARRTTDDMAGRDLGNILTILSGSER
RWMQLLAKHRAQISSAPNFGFELAVRRTSDDDMAGLDLGHVRTIVTGAER
RWLRAVSRYRAHTSGGPNFAYDLCVDRVGEDERAGLDLSGWKVAYNGAEP
RWLKTLSERRGTCSSGPNFAYELCVRKISDEQKAGLDLSSWELAFCGAEP
LWMKKAHEHKASILSSPNFGYNYFLKFLKDNKSYDWLSHIRVIANGAEP
* : : * : * : * : * : *

Orf26

gb	AAB52538.1		acyl_CoA_L		Mb
emb	CAB05426.1		fadD29		Mt
gb	AAG02359.1		blmVI		M1 Sv
gb	AAC44128.1		safB		M1 Mx
gb	AAF08795.1		MycA		M1 Bs

Orf26

gb	AAB52538.1	acyl_CoA_L	Mb
emb	CAB05426.1	fadD29	Mt
gb	AAG02359.1	blmVI	M1 Sv
gb	AAC44128.1	safB	M1 Mx
gb	AAF08795.1	MycA	M1 Bs

DPRLEDAASPALRPADP-AAAREIP---GVGRV-PDFEVLIVDPDGLRP
DTESLSAGH---AKPCAGGG-ATSLIS----YMLPRSPIVRIVSDSPTCIE
VYQQLSVGGQ---AKRAEVSSEGANLVLS---YGPRASTVRIVDPETRM
DRAALRAGR---LRPAGPGEGAGLELV---GNGTAGLDTTLRIVDPATARE
QREALAHR---AVAASSPGEAARDTVRHVSCGTVPVDEQLLVDPETRTA
HRDHLNLGE---RAVEVSKEDQNCASFVEVGKPIDYCIRICN-EANEG
.
*
.
:
:
:
:

```

Orf26
gb|AAB52538.1|acyl_CoA_L|Mb
emb|CAB05426.1|fadD29|Mt
gb|AAG02359.1|blmVI|M1|Sv
gb|AAC44128.1|safB|M1|Mx
gb|AAF08795.1|MycA|M1|Bs

```

AL6

LPEGRVGEIWLRLPGAGAGYWGRLNPGIFDARPAGDQDGGWVRL
CPDGTVEGIWVHGDNVNGYWGQKPDSERTFGGKIIVTSPSGTPEGWVRL
NPAGTVEGIWVQGDNVGLGYWRNPQQTATFRARLVTPSGTSEGWVRL
CPGGEVGEVWVRGPGVARGYFGRPRESAPLLAARLPGGEGPYLRL
LPPGGHIEGIWVRGSPVAGQGYWLRPEETARTFQARLAGGTEAPWVRL
LEDGFIGHIQIKGENVTQGGYNNPESTNRLTPDGVVKT

* : * : * : * : * : *

Orf26

gb	AAB52538.1	acyl_CoA_L	Mb
emb	CAB05426.1	fadD29	Mt
gb	AAG02359.1	blmVI	M1 Sv
gb	AAC44128.1	safB	M1 Mx
gb	AAF08795.1	MycA	M1 Bs

AL6 AL7

GDLGALTGGELFLTGRRLKELLIVHGRNLAPHDLEREARAHAHDVVDHQIGA
GDSGFVTDGKMFITGRIKDLLIVYGRNHSPDDIETIQTETGR---CA
GDLGVIFEGELFTGRIKELLIVDGRNHPDIEATIQTETGR---VV
GDLGALHDGELFLTGRHKDLIVTGRQNHHPDILERTAEQAHPALRPTCAA
GDLGFLHDGELFVSGRRKDLLVIRGRNYYPDLELTVERSHPALRPGCAA
GDLGFIRKGNLVVFGREKDIIFVGNKNVYPHDIERVAIELEDIDLGRVA
* * * * * * * * * * * * * * * * * * *

Orf26

gb AAB52538.1	acyl_CoA_L Mb
emb CAB05426.1	fadD29 Mt
gb AAG02359.1	blmVI M1 Sv
gb AAC44128.1	safB M1 Mx
gb AAF08795.1	MycA M1 Bs

```

AFGVFAP-----DERIVLVQVBHPHPTLDELPR-----VASAVSRRLTVSFGV
AISVPGDRRTEKLVAIIBLKRGDSQDDAMNLRGAIKREVSATLSSSHG
AIAVPDDR-TEKLVTTIELMKRGRTDEEEKNRLRTVKREVASAISRSRHL
AFVSPGDDG-AERVLVVCELTSYRADPAA-----VAAARRAADLAARHG
VFSVSVGGA-SEBVVVQVEVDRRYPGGDWPD-----VIAAIRDLISEQHAL
ACGVYDQETRSREIVLFAVYKKSADRFAP-----LVKDKIKKHLVQRGGW

```

```

Orf26
gb|AAB52538.1|acyl_CoA_L|Mb
emb|CAB05426.1|fadD29|Mt
gb|AAG02359.1|blmVI|M1|Sv
gb|AAC44128.1|safB|M1|Mx
gb|AAF08795.1|MycA|M1|Bs

```

AL8

```
PVRNVLVRRGIVRRRTTSGKIRRTAVRERFLAGGITALHAELEPALRPVQ
SVADLVLVAPGSIPTITSGKVRRGACVEQYRQDQPARLDA-----
RVADVVMVAPGSIPTITSGKVRRSASVERYLHHEFSRLDLMA-----
APHTLVVLRRGSIPTKTTSGKVRRGHCRTAYLDGTLFVHTAVRLP-----
RVHAVVLIKSGSLLKTTSGKVGKRGATREAYLEGQLDTSADAAQEPVGE-
SIKEILPIR--KLPKTTSGKVKIRYELAEQYESGKFALESTKIKEFLEG--
: : : * * * * *
```

Orf26
gb|AAB52538.1|acyl_CoA_L|Mb
emb|CAB05426.1|fadD29|Mt
gb|AAG02359.1|blmVI|Ml|Sv
gb|AAC44128.1|safB|M1|Mx
gb|AAF08795.1|MycA|M1|Bs

AGAGR

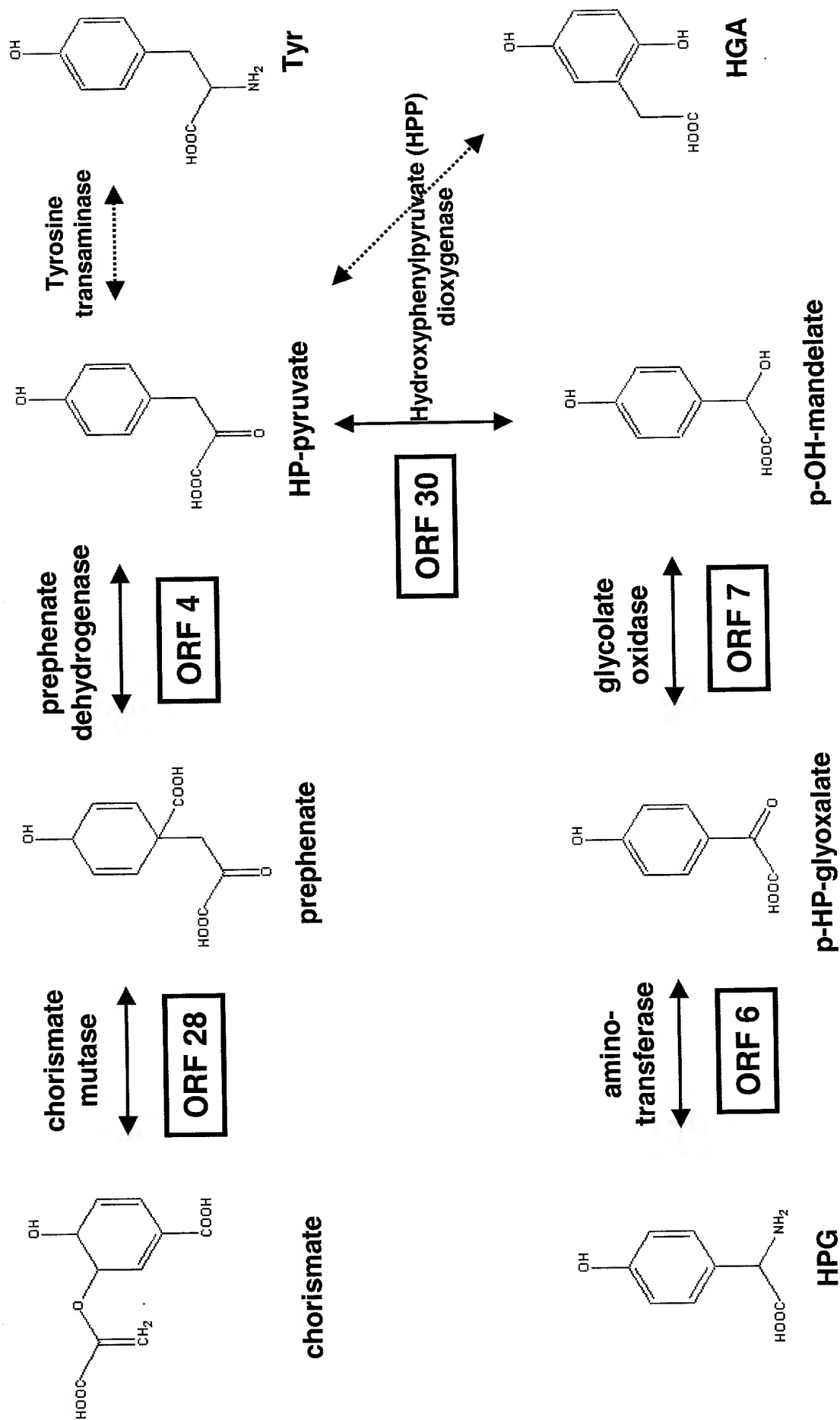


Figure 5A

pfam00753
1SML
ORF 10

LVEDDDGAALIDTGFTAPAAKALLRLLKDG--GKKIDAIILTHAHADHIGGVPELLER
LVQTPDGAVLLDGGMPQMASHLLDNMKARGVTPRDLRLILLSHAHADHAGPVAELKRR
VMQTEQAAVVTDP-FISTDNRHGDRYTLDDL-PDHIDLVLITHGHQDHIVLETLLQLR
::: :.*.: * : : : :::*.*** . * *

Figure 5B

pfam00067
ORF 10

DPE--RFLDEN-GKFKKSYAFLPFGAGPRNCLGERLARMELFLFLATLLQRFELE
DPVLYRYIRDHVGQVD-----MAFL-G-MECDGAPLNWLYKGLLTKPVNKKMSAS
** *:: :: *:. . :.* * :.* * * : * : .: :. . .

Figure 6

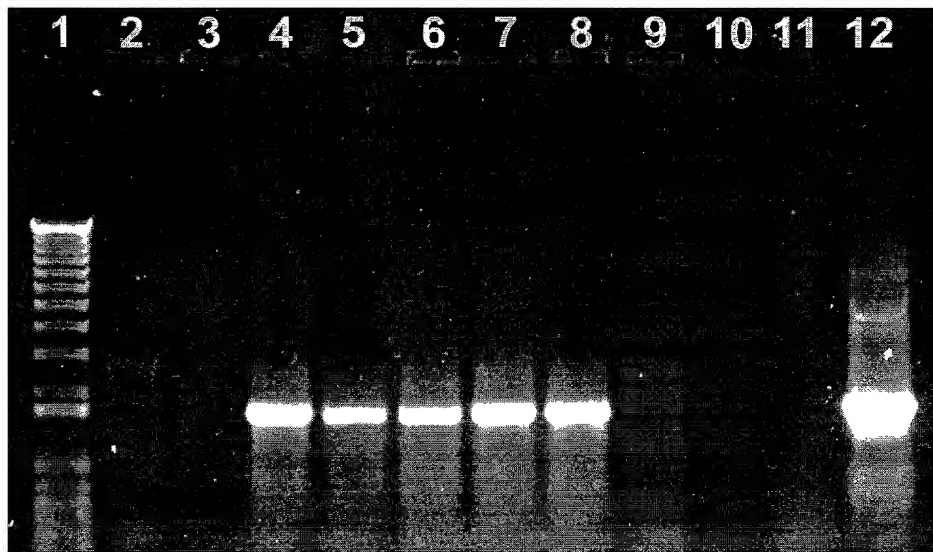


Figure 7

